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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 1951.49 Seconds

(without alignments)
11875.950 Million cell updates/sec

Title: US-09-576-424-11

Perfect score: 1431

Sequence: 1 atgaacacctgtgttctt.....ccctgtctccgggtaaatga 1431

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_estc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	63.0	1020	14	BQ062878 AGENCOURT
2	864	60.4	947	14	BQ709771 AGENCOURT
3	850.4	59.4	958	14	BQ706140 AGENCOURT
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7	824.4	57.6	1029	14	BQ063185
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9	822.2	57.5	918	14	BQ708022
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11	808.8	56.5	991	14	BQ711291
12	800.2	55.9	1031	14	BQ064886
13	797.4	55.7	936	14	BQ711727
14	796	55.6	940	14	BQ705928
15	787.4	55.0	977	14	BQ710532
16	786.4	55.0	980	14	BM914504
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19	777.2	54.3	973	14	BQ706204
20	776	54.2	930	13	BM007597
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22	764.6	53.4	926	14	BQ710304
23	764.2	53.4	917	14	BQ708169
24	759.4	53.1	961	14	BQ710233
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31	737.4	51.5	913	14	BQ707472
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33	733.8	51.3	944	14	BQ712397
34	733.6	51.3	919	14	BQ709339
35	732.8	51.2	936	14	BQ707530
36	732.4	51.2	855	13	BM007689
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40	728.8	50.9	941	14	BQ712021
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ALIGNMENTS

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DEFINITION AGENCOURT_6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
5', mRNA sequence.
ACCESSION BQ062878
VERSION BQ062878.1 GI:19890085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence start: 21
High quality sequence stop: 681.
Location/Qualifiers

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/lib_host="DH10B (phage-resistant)"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >50bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      239 a   344 c   269 g   166 t       2 others
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Best Local Similarity 98.0%; Pred. No. 4.2e-219;
Matches 923; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

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VERSION BQ706140.1 GI:21845039
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 958)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@nihs.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2464 row: a column: 01
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Location/Qualifiers
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 229 a 319 c 256 g 150 t 4 others
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Best Local Similarity 99.2%; Pred. No. 6e-206;
Matches 865; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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FEATURES
source

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: c column: 02
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
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GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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VERSION BM007892.1 GI:16522233
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 901)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
Location/Qualifiers
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT 209 a 315 c 234 g 143 t
ORIGIN
Query Match 58.1%; Score 831.2; DB 13; Length 901;
Best Local Similarity 97.7%; Pred. No. 4.6e-201;
Matches 864; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

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VERSION BO063185.1 GI:19890681
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SOURCE human.
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1029)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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using ZAP-cDNA synthesis kit (Stratagene) and Superscript
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 1 (bases 1 to 936)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
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 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
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 BASE COUNT 231 a 306 c 245 g 152 t 2 others
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GenCore version 5.1.6
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DEFINITION Sequence 11 from patent US 6113898.
ACCESSION AR108867
VERSION AR108867.1 GI:12825143
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1431)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
JOURNAL Patent: US 6113898-A 11 05-SEP-2000;

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DEFINITION Sequence 17 from patent US 6135941.
ACCESSION AR135359
VERSION AR135359.1 GI:14476031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1567)
AUTHORS Hillman, J. L., Lal, P., Tang, Y. Tom., Yue, H., Au-Young, J.,
Corley N. C., Guegler, K. J. and Baughn, M. R.
TITLE Human immune system associated molecules
JOURNAL Patent: US 6135941-A 17 24-Oct-2000;
FEATURES Location/Qualifiers
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RESULT 7
AK057775
LOCUS
DEFINITION
Homo sapiens cDNA FLJ25046 fis, clone CBL03624, highly similar to
Ig gamma immunoglobulin heavy chain.
ACCESSION
AK057775
VERSION
AK057775.1 GI:16553709
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M.,
Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
Sugano,S.
NEDO human cDNA sequencing project
TITLE
NEDO human cDNA sequencing project
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1589)
Sugano,S. and Suzuki,Y.
Direct Submission
Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
LOCATION/Qualifiers
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Best Local Similarity 93.0%; Pred. No. 7.8e-240;
Matches 1334; Conservative 0; Mismatches 82; Indels 18; Gaps 3;
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Db 38 ATGAAGCAGATGTGTTCTTCTCTCTCTGTGGGAGCTCCAGATGGTCTCTGTCCCG 97
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QY 133 GGTGGCTCCATCAGCGGTGGTTATGCTGGGCTGGATCGGCCAGCGCCCGCAGGAGGGG 192
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QY 193 CTGGAGTGGATTGGGAGTTCTATAGTAGTAGTGGGAACAACCTACTACAAACCCCTCCCTC 252
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RESULT 9
LOCUS ARI176296 1418 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6312690.
ACCESSION ARI176296
VERSION ARI176296.1 GI:17918651
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1418)
AUTHORS Edelman,L., Margairite,C., Kaczorek,M. and Chaabihi,H.
TITLE Monoclonal recombinant anti-rhesus D (D7C2) antibody
JOURNAL Patent: US 6312690-A 7 06-NOV-2001;
FEATURES
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Query Match 84.8%; Score 1213.6; DB 6; Length 1418;
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Matches 1312; Conservative 0; Mismatches 94; Indels 12; Gaps 3;
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LOCUS AR135375 1404 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 7 from patent US 6136310.
ACCESSION AR135375
VERSION AR135375.1 GI:14476047
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Hanna, N., Newman, R., Anthony, and Reff, M. Elliot.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 7/24-OCT-2000;
FEATURES
Location/Qualifiers
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BASE COUNT 312 a 448 c 377 g 267 t
ORIGIN

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Best Local Similarity 90.4%; Pred. No. 1.5e-228;
Matches 1294; Conservative 0; Mismatches 110; Indels 27; Gaps 2;

Qy 1 ATGAAACACCTGTGGTTCTTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCTCCAG 60
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RESULT 13
AR135376 LOCUS AR135376 1404 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 9 from patent US 6136310.
ACCESSION AR135376
VERSION AR135376.1 GI:14476048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Hanna, N., Newman, R., Anthony, and Reff, M., Elliot.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 9 24-OCT-2000;
FEATURES
source Location/Qualifiers
1..1404
BASE COUNT 313 a 446 c 379 g 266 t
ORIGIN

Query Match 82.2%; Score 1176.2; DB 6; Length 1404;
Best Local Similarity 90.2%; Pred. No. 1.4e-227;
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Db 1234 AAGACACGCTCCCGTGTGAGCTCCGACGGCTCCTTCTCTACAGCAAGCTCAC 1293
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QY 1321 GTGGACAAGAGCGTGGCAGCAGGGAAGCTTCTTCATGCTCCGTGATGATGAGGCT 1380
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 QY 1381 CTGCACAACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGGTAATGA 1431
 Db 1354 CTGCACAACCACTACACAGAGAGCCTCTCCCTGTCTCCGGGTAATGA 1404

RESULT 14

BC024289
 LOCUS 1630 bp mRNA linear PRI 28-FEB-2002
 DEFINITION Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.

BC024289
 VERSION BC024289.1 GI:18999464

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1630)

Strausberg, R.

Direct Submission

Submitted (26-FEB-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Len Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 42 Row: 0 Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Genomescan gene prediction, Similarity but not identity
 to protein.

FEATURES

source

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DEFINITION	Sequence 17 from patent US 5866125.					
ACCESSION	AR031184					
VERSION	AR031184.1 GI:5945473					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1428)					
AUTHORS	Brams, P., Chamat, S. Salim., Pan, L.-Z., Walsh, E. E., Heard, C. Janne.					
TITLE	Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof					
JOURNAL	Patent: US 5866125-A 17 02-FEB-1999;					
FEATURES	Location/Qualifiers					
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ORIGIN	/organism="unknown"					
Query Match 79.3%; Score 1134.8; DB 6; Length 1428;						
Best Local Similarity 89.08; Pred. No. 3.2e-219;						
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;						
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Search completed: June 3, 2003, 17:50:57
Job time : 3717.97 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 319.784 Seconds
(without alignments)
10077.457 Million cell updates/sec

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Perfect score: 1431
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18	Primates anti-hu
2	1431	100.0	1431	19	Macaque primatized
3	1431	100.0	1431	24	DNA sequence of a
4	1315.8	91.9	1431	18	Primates anti-hu
5	1315.8	91.9	1431	19	Macaque primatized
6	1315.8	91.9	1431	24	DNA sequence of a
7	1276.4	89.2	1567	22	Human immune syste
8	1261.2	88.1	1431	17	Monoclonal antibody
9	1261	88.1	1634	21	Human immune syste

10	1224.8	85.6	1418	17	Anti-rhesus D reco
11	1181	82.5	1404	18	Human gamma-4 heav
12	1177.8	82.3	1404	18	Human gamma-4PE he
13	1176.2	82.2	1404	18	Human gamma-4E hea
14	1151	80.4	1428	22	Nucleotide sequenc
15	1136.4	79.4	1428	18	Human anti-RSV mon
16	1134	79.2	1430	24	cDNA of the heavy
17	1134	79.2	1644	22	Human cDNA encodin
18	1133.8	79.2	1507	21	Human immunoglobul
19	1133.4	79.2	1798	21	Human colon cancer
20	1123.6	78.5	1428	18	Human anti-RSV mon
21	1122.8	78.5	1599	24	Human benign prost
22	1122.8	78.5	1599	24	Colon adenocarcino
23	1122.8	78.5	1599	24	Lung cancer relate
24	1122.8	78.5	1599	24	Lung cancer relate
25	1121.2	78.4	1617	14	Antibody D heavy c
26	1120.8	78.3	19035	19	Traget plasmid Man
27	1119.6	78.2	1549	13	Encodes heavy chai
28	1119	78.2	1442	22	Plasmid Glambda-1B
29	1118	78.1	1449	20	Monoclonal antibod
30	1118	78.1	1449	20	Monoclonal antibod
31	1115.8	78.0	6281	22	Plasmid Glambda-1A
32	1112.4	77.7	1437	19	Macaque primatized
33	1112.4	77.7	1437	24	DNA sequence of a
34	1110.8	77.6	1427	19	Plasmid H19Hcpd
35	1110.8	77.6	1427	19	Plasmid H19Hcpd
36	1110.8	77.6	1437	18	Primates anti-hu
37	1109.8	77.6	1458	13	Reshaped CD4 antib
38	1109.8	77.6	1458	13	Plasmid H19Hcpd
39	1109.2	77.5	1427	19	Plasmid H19Hcpd
40	1107.8	77.4	1576	14	Human anti-HBs hea
41	1102.8	77.1	6284	19	Plasmid H19Hcpd
42	1102.2	77.0	6557	17	Anti-IgE VH expres
43	1101	76.9	1431	22	Chimeric 4H6 anti-
44	1101	76.9	1431	22	Chimeric 4H6 anti-
45	1100.8	76.9	2912	22	Human cDNA encodin

ALIGNMENTS

RESULT 1
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ID AAT62513 standard; DNA; 1431 BP.

AC AAT62513;
XX AC
XX 25-MAY-1997 (first entry)

Primates anti-human B7.1 antigen antibody 16C10 heavy chain DNA.

Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
Primates antibody; B7 antigen; CD28; immunosuppressive;
autoimmune disease; idiopathic thrombocytopenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
type 1 diabetes mellitus; graft versus host disease;
hetero-hybridoma; transfectoma; ss.

Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.

WO9640878-A1.

19-DEC-1996.

06-JUN-1996; 96WO-US10053.

07-JUN-1995; 95US-0487550.

(IDEC-) IDEC PHARM CORP.

Anderson DR, Brans P, Hanna N, Shestowsky WS;

XX

QY 238 TACAACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCGAAGAACAGTTC 297
DB 315 TACAACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCGAAGAACAGTTC 374
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QY 358 GCTCTTTTTCAGTTGTTGGAATGTTTAAACAACACTGGTTCGATGTCTGTGGGCCCGGGA 417
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DB 846 GCACCTGAATCTCTGGGGGACCGTCAAGTCTTCTTCTTCCCTCCCAAAACCAAGACAC 905
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QY 958 CCGCGGAGGAGGATGACAAAGCAGCTACCGTGTGCTGAGCGTCTCAGCTGTGAC 1017
DB 1026 CCGCGGAGGAGGATGACAAAGCAGCTACCGTGTGCTGAGCGTCTCAGCTGTGAC 1085
QY 1018 CAGGACTGCTGAATGGCAAGAGTACAGTCAAGTCTCAACAAAGCCCTCCAGCC 1077
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DB 1386 ACCGTGGAACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCGTGCATGAG 1445
QY 1378 GCTCTGCAACCACTACACGCAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
DB 1446 GCTCTGCAACCACTACACGCAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1499

RESULT 8
AAT18059
ID AAT18059 standard; DNA; 1431 BP.
XX
AC AAT18059;
XX
DT 16-AUG-1996 (first entry)
XX Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
DE Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1428
FT /tag= a
FT sig_peptide 1..57
FT /tag= b
FT mat_peptide 58..1425
FT /tag= c
FT 3'UTR 1426..1431
FT /tag= d
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XX JP08038178-A.
XX
XX PN 13-FEB-1996.
XX
XX PD 20-FEB-1995; 95JP-0030742.
XX
XX PR 18-FEB-1994; 94JP-0021628.
XX
XX (NISN) NISSHINBO IND INC.
XX (TANA/) TANAKA H.
XX
XX WPI; 1996-154852/16.
XX
XX DR P-PSDB; AAR93553.
XX
XX PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
XX produced by primer amplification, used in the diagnosis of hCMV
XX infection
XX
XX PS Claim 6; Page 16-18; 22pp; Japanese.
XX
XX CC The sequences given in AAT18059-60 encode the heavy and light chains
XX respectively of a monoclonal antibody against a 65 kD antigen of human
XX cytomegalovirus (hCMV). These sequences were amplified using the
XX sequences given in AAT18040-58. The monoclonal antibody may be used
XX in the diagnosis of hCMV.
XX
XX SQ Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T; 0 other;

Query Match 88.1%; Score 1261.2; DB 17; Length 1431;
Best Local Similarity 93.9%; Pred. No. 8.6e-251;
Matches 1347; Conservative 0; Mismatches 78; Indels 9; Gaps 3;

QY 1 ATGAACACCTGTGTGTTCTTCTCTCTCTGTGGAGCTCCAGATGGTCTCTGTCCAG 60
DB 1 ATGAAGCATCTTGTGTTCTTCTCTCTCTGTGGAGCTCCAGATGGTCTCTGTCCAG 60
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DB 61 CTGAGCTGCGAGAGTCGGGCCCGAGAGCTGTGTAAGCTTCGAGACCTGTCCCTCACC 120

121 TGGCTGTCTCTGGTGGCTCCATCAGC---GGTGGTATGGCTGGGCTGGATCCGCCAG 177
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RESULT 9
AAZ50012
ID AAZ50012 standard; cDNA; 1634 BP.
XX
AC AAZ50012;
XX
DT 25-APR-2000 (first entry)
XX
DE Human immune system molecule, ISMO-2 cDNA.
XX
KW Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW treatment; prevention; cell proliferation; immune system disorder; ss.
XX
OS Homo sapiens.
XX
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FT FT /note= "ISMO-2 shows homology to vertebrate
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PN WO20000608-A2.
XX
PD 06-JAN-2000.
XX
PF 21-JUN-1999; 99WO-US13995.
XX
PR 30-JUN-1998; 98US-0107223.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
PI Baughn MR;
XX
DR WPI; 2000-170916/15.
DR P-P5DB; AAY44721.
XX
PT Immune system molecules used in the diagnosis, treatment and prevention
PT of disorders associated with the immune system and cell proliferation
XX
PS Claim 7; Pages 64-65; 69pp; English.
XX
CC The present sequence is a cDNA encoding an immune system molecule,
CC ISMO-2 from an Incyte clone 2849752 isolated from the human breast
CC tumour cDNA library (BRSTUT13). This sequence is expressed in several
CC libraries, generally those associated with cancer, cell
CC proliferation, immune response or trauma.


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QY 1391 ACACGAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA 1428
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Job time : 324.784 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 188.659 Seconds
(without alignments)
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Title: US-09-576-424-11

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1431	100.0	1431	9	US-09-948-429B-11
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4	1315.8	91.9	1431	9	US-10-124-905-3
5	1315.8	91.9	1431	9	US-09-948-429B-3
6	1314.2	91.8	1431	9	US-10-073-138-2
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9	1176.2	82.2	1404	9	US-10-211-357-9
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Sequence 14, Appl
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Sequence 87, Appl
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Sequence 20, Appl
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25 1100.4 76.9 1356 10 US-09-823-698A-27
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36 1089.2 76.1 1347 10 US-09-736-371B-20
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39 1088.6 76.1 1640 10 US-09-822-849A-321
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45 1086 75.9 1605 10 US-09-822-830A-501

ALIGNMENTS

RESULT 1

US-10-124-905-11
; Sequence 11, Application US/10124905
; Patent No. US20020166136A1

; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1431 base pairs

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; Sequence 11, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF,
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:

RESULT 2
US-09-948-429B-11
Sequence 11, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIVATIZED FORMS THEREOF,
AND USE THEREOF AS
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

RESULT 3

APPLICANT: ANDERSON, Darrell R.

HANNA, Nabil
BRAMS, Peter

TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND B7.2 CO-STIMULATORY ANTIGENS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOA
STREET: P. O. BOX 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United
ZIP: 22313-1404

ZIP: 22313-1404
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
PC DOS/MS
DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.30

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RESULTS

US-10-211-357-11
Sequence 11, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and

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Db 994 GACTGCTCAAGCGCAAGAGTACAGTCAAGTCTCAAGAGTCTCAAGAGTCTCAAGAGTCTCC 1053
Qy 1081 ATCGAGAAACCATCTTCCAAAGCCAAAGCGACGCCCGGAGAACCAAGTGTACACCTGT 1140
Db 1054 ATCGAGAAACCATCTTCCAAAGCCAAAGCGACGCCCGGAGAACCAAGTGTACACCTGT 1113
Qy 1141 CCCCCATCCCGGAGT 1200
Db 1114 CCCCCATCCCGGAGT 1173
Qy 1201 TTCTATCCAGCAGATCCCGT 1260
Db 1174 TTCTATCCAGCAGATCCCGT 1233
Qy 1261 AAGACACACCTCCCGT 1320
Db 1234 AAGACACACCTCCCGT 1293
Qy 1321 GTGGACAAGCAGT 1380
Db 1294 GTGGACAAGCAGT 1353
Qy 1381 CTGCACAACCTACACGAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1431
Db 1354 CTGCACAACCTACACGAGAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1404

RESULT 10

US-09-740-002-17
; Sequence 17, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-027579
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 1428

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(1425)
US-09-740-002-17

Query Match 79.3%; Score 1134.8; DB 10; Length 1428;
Best Local Similarity 89.0%; Pred. No. 1.2e-304;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;

Qy 17 TCTTCT 76
Db 17 TCTTCT 76
Qy 77 CGGGCCCCAGGACTGTGTGAAGCCTTCGGAGACCCCTGTCCCTCACTCCGCGCTGTCTCTGGTG 136
Db 77 CTGTGCTCTGTGTGTGTGAACCCACAGAGACCCCTCAGCTGACCTGCACCGTCTCTGGGT 136
Qy 137 GCTC---CATCAGCGGTGTGTATGCTGGGGTGTGATCCGCCAGCCCCCAGGGAAGGGGC 193
Db 137 TCTCACTCAGCAACCTAGAAATGGGTGTGACCTGGATCCGTGAGCCCCCAGGGAAGGGCC 196
Qy 194 TGGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTACACCCCTCCCTCA 253
Db 197 TAGAATGGCTTGGAAACATTTTTCGAGTGTGACGAA---GTCCCTTCAGTCTCTCTCTGA 253
Qy 254 AGAGTCAAGTCAACATTTCAACAGACAGCTTCAAGAACCCAGTTCCTCCCTGAAAGCTGAACT 313
Db 254 AGAGCAGACTCAACCTCCAGGACACCTCCAGAGCCAGGTGTCTTAAGCTTGACCA 313
Qy 314 CTATGACCGCCGACGACCGCGGTATTTACTGTGTGAGAGATCGTCTTTTTCAGTTG 373
Db 314 ACGTGGACCTGTGGACACAGCACATATTTACTGTGACCGGTAGGACTGTATGACATCA 373
Qy 374 TTGGAAATGGTTTACAACTGTTCGATGTCTGGGGCCCGGAGTCTCTGGTCAACGCTCT 433
Db 374 ATGCTT---ATTACCTATATCTACCTGGATTTATTGGGGGAGGAAACCTCTGGTCAACGCTCT 430
Qy 434 CTTCACTAGTACCAAGGCGCCATCGTCTTCCCTTGGCACCTCTCTCAAGAGCACCT 493
Db 431 CTTCACTAGTACCAAGGCGCCATCGTCTTCCCTTGGCACCTCTCTCAAGAGCACCT 490
Qy 494 TTGGGGGACACGCGCCCTGGGCTGCTTGTCAAGGACTACTTCCCGAACCGGTGACCG 553
Db 491 CTGGGGGACACGCGCCCTGGGCTGCTTGTCAAGGACTACTTCCCGAACCGGTGACCG 550
Qy 554 TGTCTGTGAACTCAGCGCCCTGACAGCGGCTGACACCTTCCCGGCTGTCTTACAGT 613
Db 551 TGTCTGTGAACTCAGCGCCCTGACAGCGGCTGACACCTTCCCGGCTGTCTTACAGT 610
Qy 614 CTTCAAGGACTTACTCTCTCAGCAGCTGTGACCGTCCCTTCCAGCAGCTTTGGGACCC 673
Db 611 CTTCAAGGACTTACTCTCTCAGCAGCTGTGACCGTCCCTTCCAGCAGCTTTGGGACCC 670
Qy 674 AGACCTTACATCTGCAACCTGTGAATCAAGCCCAAGCAACCAAGGTGGAAGAAAGCAG 733
Db 671 AGACCTTACATCTGCAACCTGTGAATCAAGCCCAAGCAACCAAGGTGGAAGAAAGCAG 730
Qy 734 AGCCCAATCTTGTGACAAACTCACAATGCCACCGTGGCCAGCAGCTTGAACCTCTGG 793
Db 731 AGCCCAATCTTGTGACAAACTCACAATGCCACCGTGGCCAGCAGCTTGAACCTCTGG 790
Qy 794 GGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 853
Db 791 GGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 850
Qy 854 CCCCCTGAGGTCAATGCGGT 913
Db 851 CCCCCTGAGGTCAATGCGGT 910
Qy 914 ACTGTGACGCGGT 973

Db 1182 AGTGAAGGTCTCCAAACAAGCCCTCCAGAGCCCATCGAGAAAACCATCTCAAGACA 1241
QY 1106 AAGGGCAGCCCGAGAACACAGGTGTACACCTGCCGCCATCCCGGGATGAGCTGACCA 1165
Db 1242 AAGGGCAGCCCGAGAACACAGGTGTACACCTGCCGCCATCCCGGGAKGAGMTGACCA 1301
QY 1166 AGAACAGGTGAGCTGAGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGGTGG 1225
Db 1302 AGAACAGGTGAGCTGAGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGGTGG 1361
QY 1226 AGTGGAGAGCAATGGGAGCGGAGAACAACTACAGAACACAGCTCCCGTGGACT 1285
Db 1362 AGTGGAGAGCAATGGGAGCGGAGAACAACTACAGAACACAGCTCCCGTGGACT 1421
QY 1286 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGACAGAGCAGGTGGCAGCAGG 1345
Db 1422 CCGACGGCTCTTCTCTCTAYAGCAAGCTCACCGTGACAGAGCAGGTGGCAGCAGG 1481
QY 1346 GGAACGTCTTCTATGCTCCGTGATGATGAGCTCTGCACAACTACAGCAAGCA 1405
Db 1482 GGAACGTCTTCTATGCTCCGTGATGATGAGCTCTGCACAACTACAGCAAGCA 1541
QY 1406 GCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1542 GCTCTCCCTGTCTCCGGGTAAATGA 1567

RESULT 13

US-09-740-002-19
; Sequence 19, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1425)
US-09-740-002-19

Query Match 78.6%; Score 1125.2; DB 10; Length 1428;
Best Local Similarity 88.6%; Pred. No. 5.3e-302;
Matches 1256; Conservative 0; Mismatches 153; Indels 9; Gaps 3;

QY 17 TCTTCTCTCTCTGTTGGGAGCTCCAGATGGTCTGTCCAGGTGACGTGACAGGAGT 76
Db 17 TCTTGTCTCTCTGTTGGTGTGTACCGGTGTCTTGTCCAGGTGACAGTTCAGGAGT 76
QY 77 CGGGCCAGGACTGGTGAAGCTTCCGAGACCTGTCCCTCACCTGCGTGTCTCTGGTG 136
Db 77 CTGTCCTGGTGTGTAAACCCACACAGACCTCTACACTGACCTTCTCTGGGT 136
QY 137 GCTC---CATCAGCGGTGTTATGGCTGGGCTGGATCCGACGCCGCCAGGGAAGGGC 193
Db 137 TCTCACTCAGCACAGAGGAATGAGTGAATGGATCGTTCAGCCCCCAGGGAAGGCC 196
QY 194 TGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGACACCTACTACAAACCCCTCCTCA 253

Db 197 TGGAAATGCTAGCCCGCAATTGATTGGGACGATG---ATACATTCTACAGCGCTTCTCTGA 253
QY 254 AGAGTCAAGTCAACATTTTCAACAGACACGTCACAGAACACAGTTCTCCCTGAAGCTGAAC 313
Db 254 AGACTAGCTCAGCATCTCCAGGACACCTCCAAAACACAGGTGGTCTCAGAAATGACCA 313
QY 314 CTATAGCCGCGCGGACACGCGGTGTATTAATCTGTGTGAGAGATCGTCTTTTTCAGTTG 373
Db 314 ACGTAGACCTGTGTGACACAGCCACATATTTTGTGCACGGGCTCTCATATAT---GACA 370
QY 374 TTGGAATGGTTTACAAACAATCGTTTCGATGTCTGGGCGCCGAGGTCTCTGGTACCGTCT 433
Db 371 GTGATAGTTTCTTACCTCTTCTACATGCTTCTGGGGCCAGGGAACCGTGGTCAACGCT 430
QY 434 CCTAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCCGCAACCTCTCTCCAAAGACACCT 493
Db 431 CCTAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCCGCAACCTCTCTCCAAAGACACCT 490
QY 494 CTGGGGGACACAGCGGCCCTGGGCTGCTGTGTCAAGGAATCTTCTCCCGAAACCGGTGACGG 553
Db 491 CTGGGGGACACAGCGGCCCTGGGCTGCTGTGTCAAGGAATCTTCTCCCGAAACCGGTGACGG 550
QY 554 TGTCTGTGAATCTCAGGCGCCCTGACCGAGGGGTGACACCTTCCCGGCTGTCTACAGT 613
Db 551 TGTCTGTGAATCTCAGGCGCCCTGACCGAGGGGTGACACCTTCCCGGCTGTCTACAGT 610
QY 614 CCTCAGGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTGTCCCTCCAGCAGCTTGGCACC 673
Db 611 CCTCAGGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTGTCCCTCCAGCAGCTTGGCACC 670
QY 674 AGACTCATCTGTCAACCGTGAATCAAGGCCAGCAACCAAGGTGACAAAGGAGCAG 733
Db 671 AGACTCATCTGTCAACCGTGAATCAAGGCCAGCAACCAAGGTGACAAAGGAGCAG 730
QY 734 AGCCCAATCTGTGACAAACTCACAATGCCACCGTGTCCCGACACCTCATGATCTCCCGGA 793
Db 731 AGCCCAATCTGTGACAAACTCACAATGCCACCGTGTCCCGACACCTCATGATCTCCCGGA 790
QY 794 GGGACCCCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGA 853
Db 791 GGGACCCCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGA 850
QY 854 CCCCTGAGGTCAATGCTGTGTGTGAGCGTGTGAGCCAGAGACCCCTGAGGTCAAGTTCA 913
Db 851 CCCCTGAGGTCAATGCTGTGTGTGAGCGTGTGAGCCAGAGACCCCTGAGGTCAAGTTCA 910
QY 914 ACTGTGACGTGAGCGGTGTGAGGTGCTATATGCCAAGACAAAGCCGCGGAGGAGCAGT 973
Db 911 ACTGTGACGTGAGCGGTGTGAGGTGCTATATGCCAAGACAAAGCCGCGGAGGAGCAGT 970
QY 974 ACAACAGCACCTACCGTGTGTGTGAGCGTCTCACCGTCTGACAGGACTGGCTGAATG 1033
Db 971 ACACAGCACCTACCGTGTGTGTGAGCGTCTCACCGTCTGACAGGACTGGCTGAATG 1030
QY 1034 GCAAGGAGTACAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCATCGAGAAAACA 1093
Db 1031 GCAAGGAGTACAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCATCGAGAAAACA 1090
QY 1094 TCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCGCCATCCCGGG 1153
Db 1091 TCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCGCCATCCCGGG 1150
QY 1154 ATGAGCTCACCAAGAACACAGGTGTGAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1213
Db 1151 ATGAGCTGACCAAGAACACAGGTGTGAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1210
QY 1214 ACATGCGGTGAGGTGGAGAGCAATGGGACGCGGAGAACAACTAAGACCAAGCAGCCTC 1273
Db 1211 ACATGCGGTGAGGTGGAGAGCAATGGGACGCGGAGAACAACTAAGACCAAGCAGCCTC 1270
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Db 1271 CCGTGTGAGTCCGAGCGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCA 1330

QY 1334 GGTGGCAGCAGGGAAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACT 1393
DB 1331 GGTGGCAGCAGGGAAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACT 1390
QY 1394 ACACGACAGAGAGCCCTCCCTGTCTCCGGGTAATGA 1431
DB 1391 ACACGACAGAGAGCCCTCCCTGTCTCCGGGTAATGA 1428

RESULT 14
US-09-954-456-789
; Sequence 789, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 789
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-789

Query Match 78.5%; Score 1122.8; DB 10; Length 1599;
Best Local Similarity 87.8%; Pred. No. 2.5e-301;
Matches 1249; Conservative 0; Mismatches 167; Indels 6; Gaps 2;

QY 13 TGTATGACGCGCGGACACGCGCGGTATTTACTGTGTGAGAGATCG---TCTTTTTC 369
DB 1344 AGCCTGAGATCTGAGGACACGCGCGGTATTTACTGTGTGAGAGATCGTGTACAGGACG 403
QY 370 GTTGTGTAATGTTTACAAACAACTGGTTTCGATGTCTGGGGCCCGGGAGTCTCTGTGTCACC 429
DB 404 AATTTTGACCGGGCCCGGGTTGGCTTGGTTTGACCCCTGGGGCCAGGGACACCTGTGTGTCACC 463
QY 430 GTTCTCTCAGCTAGACCAAGGGCCCATCGGTTCTTCCCTCTGGGCAACCTCTCTTCCAGAGC 489
DB 464 GTTCTCTCAGCTTCCCAAGGGCCCATCGGTTCTTCCCTCTGGGCAACCTCTCTTCCAGAGC 523
QY 490 ACTCTGTGGGGCACAGCGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 549
DB 524 ACTCTGTGGGGCACAGCGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 583
QY 550 ACGGTGTCTGTGAACTCAGAGGGCCCTGACACGCGGCTGACACACCTTCCCGGCTGTCTTA 609
DB 584 ACGGTGTCTGTGAACTCAGAGGGCCCTGACACGCGGCTGACACACCTTCCCGGCTGTCTTA 643
QY 610 CAGTCTCAGGACTCTACTTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGGC 669
DB 644 CAGTCTCAGGACTCTACTTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGGC 703
QY 670 ACCCAGACTTACATCTGCAACGCTGAATCACAAGCCAGCAACACCAAGGTGGACAGAAA 729
DB 704 ACCCAGACTTACATCTGCAACGCTGAATCACAAGCCAGCAACACCAAGGTGGACAGAAA 763
QY 730 GCAGAGCCCAATCTTGTGACAAAACCTCACAATGCCACCGTGCACAGCACTCAATCTC 789
DB 764 GTTGTGACCCCAATCTTGTGACAAAACCTCACAATGCCACCGTGCACAGCACTCAATCTC 823
QY 790 TTGGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAGGACACCTCTCATGTCTC 849
DB 824 TTGGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAGGACACCTCTCATGTCTC 883
QY 850 CGGACCCCTCAGGCTCAGT 909
DB 884 CGGACCCCTCAGGCTCAGT 943
QY 910 TTCAACTGTGTAGT 969
DB 944 TTCAACTGTGTAGT 1003
QY 970 CAGTACAAACAGCAGTACCGT 1029
DB 1004 CAGTACAAACAGCAGTACCGT 1063
QY 1030 AATGCAAGGAGTACAGT 1089
DB 1064 AATGCAAGGAGTACAGT 1123
QY 1090 ACCATCTCAAGCCCAAGGGCAGCCCGAGAACACACAGGTGTACACCTTGCCTCCATCC 1149
DB 1124 ACCATCTCAAGCCCAAGGGCAGCCCGAGAACACACAGGTGTACACCTTGCCTCCATCC 1183
QY 1150 CGGATGTAGCTGACCAAGAACACAGGT 1209
DB 1184 CGGATGTAGCTGACCAAGAACACAGGT 1243
QY 1210 AGCAGATCGCGGT 1269
DB 1244 AGCAGATCGCGGT 1303
QY 1270 CCTCCGCTGTGAGTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGTGACAG 1329
DB 1304 CCTCCGCTGTGAGTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGTGACAG 1363
QY 1330 AGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1389
DB 1364 AGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1423
QY 1390 CACTACGCGAGAGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1431

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
5376.898 Million cell updates/sec

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Perfect score: 1431
Sequence: 1 atgaacacctgtgttctt.....ccctgtctcgggtaataga 1431

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PTUS COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1431	100.0	1431	3	US-08-487-550-11
2	1315.8	91.9	1431	3	US-08-487-550-3
3	1276.4	89.2	1567	3	US-09-049-672A-17
4	1213.6	84.8	1418	4	US-08-793-450-7
5	1181	82.5	1404	3	US-08-523-894-7
6	1177.8	82.3	1404	3	US-08-523-894-11
7	1176.2	82.2	1404	3	US-08-523-894-9
8	1134.8	79.3	1428	1	US-08-488-376-17
9	1134.8	79.3	1428	2	US-08-634-223-17
10	1134.8	79.3	1428	2	US-08-634-223-17
11	1134.8	79.3	1428	2	US-08-634-400-17
12	1134.8	79.3	1428	2	US-08-635-878-17
13	1134.8	79.3	1428	2	US-08-770-057-17
14	1134.8	79.3	1428	4	US-09-335-697B-17
15	1134.8	79.3	1428	4	US-09-335-697B-17
16	1125.2	78.6	1428	1	US-08-488-376-19
17	1125.2	78.6	1428	2	US-08-634-223-19
18	1125.2	78.6	1428	2	US-08-634-224-19
19	1125.2	78.6	1428	2	US-08-634-400-19
20	1125.2	78.6	1428	2	US-08-635-878-19
21	1125.2	78.6	1428	2	US-08-770-057-19
22	1125.2	78.6	1428	4	US-09-335-697B-19
23	1125.2	78.6	1428	4	US-09-335-697B-19
24	1121.2	78.4	1617	2	US-08-378-939-9
25	1118	78.1	19040	4	US-09-343-485A-3
26	1112.4	77.7	1437	3	US-08-487-550-7
27	1107.8	77.4	1576	1	US-08-157-101A-6

28	1102.2	77.0	6557	1	US-08-286-740-3	Sequence 3, Appli
29	1102.2	77.0	6557	5	PCT-US95-09576-3	Sequence 3, Appli
30	1097.8	76.7	1350	1	US-08-157-101A-9	Sequence 9, Appli
31	1096.6	76.6	9209	1	US-08-149-099C-3	Sequence 3, Appli
32	1096.6	76.6	9209	1	US-08-476-275-2	Sequence 2, Appli
33	1096.6	76.6	9209	4	US-08-478-967A-3	Sequence 3, Appli
34	1096.6	76.6	9209	2	US-08-475-815B-3	Sequence 3, Appli
35	1096.6	76.6	18986	2	US-08-813-866-2	Sequence 2, Appli
36	1096.6	76.6	18986	2	US-09-023-715-2	Sequence 2, Appli
37	1096.6	76.6	18986	4	US-09-343-485A-2	Sequence 2, Appli
38	1093.8	76.4	8120	3	US-09-027-449-68	Sequence 68, Appl
39	1093.8	76.4	8120	3	US-09-026-985-68	Sequence 68, Appl
40	1093.8	76.4	8120	4	US-09-121-952A-68	Sequence 68, Appl
41	1093.8	76.4	8120	4	US-09-234-340A-21	Sequence 21, Appl
42	1069	74.7	1655	3	US-09-049-672A-11	Sequence 49, Appl
43	1051.2	73.5	6285	1	US-08-467-420A-49	Sequence 49, Appl
44	1051.2	73.5	6285	1	US-08-470-110A-49	Sequence 49, Appl
45	1051.2	73.5	6285	1	US-08-667-769A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-11
; Sequence 11, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
US-08-487-550-11

Query Match 100.0%; Score 1431; DB 3; Length 1431;

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1021	GACTGGCTGAATGGCAAGGAGTACAAAGTGTCAAGT	CTCCAAACAAAGCCCTCCAGAGCCCCC	1080
1021	GACTGGCTGATGGCAAGGAGTACAAAGTGTCAAGT	CTCCAAACAAAGCCCTCCAGAGCCCCC	1080
1081	ATCGAGAAACCATCTCCAAAGCCAAAGGCGCCGAG	AAACACACAGGTGTACACCCCTG	1140
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1141	CCCCCATCCCGGATGAGCTGACCAAGAACCAAGT	CAGCCTGACCTGCCTGGTCAAGGC	1200
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1201	TTCTATCCAGCGACATCGCCGTGGAGTGGGAGAG	CAATGGCGAGCGGAGAACTAC	1260
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1261	AGACACAGCCTCCCGTGTGGATCTCGAGCGGTCT	CTTCTTCCTCTACAGAGCTCACC	1320
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1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAGAGCT	TTCTCATGCTCCGTGTCATGAGCT	1380
1321	GTGGACAAGAGCAGGTGGCAGCAGGGGAGAGCT	TTCTCATGCTCCGTGTCATGAGCT	1380
1381	CTGCACAACCACTACACGAGAGAGCCTCTCCCT	GTCTCCGGGTAAATGA	1431
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RESULT 3

US-09-049-672A-17

; Sequence 17, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yue, Henry

; APPLICANT: Au-Young, Janice

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: PastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; FILING APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:


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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
; CHROMOSOME/SEGMENT: 4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1404
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1404
;
; US-08-523-894-7
;
; Query Match 82.5%; Score 1181; DB 3; Length 1404;
; Best Local Similarity 90.4%; Pred. No. 1.3e-275;
; Matches 1294; Conservative 0; Mismatches 110; Indels 27; Gaps 2
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; Db 61 GTGCAGCTCAGAGTTCGGGCCAGGACTGTGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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; Qy 121 TGGCGTGTCTCTGGTGGTCCATCAGCGTGGTTATGGCTGGGGCTCGATCCGCCAGGCC 180
; Db 121 TGCAGTGTCTCTGGTGGTCCATCAGCGTGACTATTATTGGTTCTGGATCCGCCAGTCC 180
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; Qy 181 CCAGGGAAGGGCTCGAGTGGATTGGGAGTTTCTATAGTAGTAGTGGGAACACTTACTAC 240
; Db 181 CCAGGGAAGGGCTCGAGTGGATCGGTACATCTATGGCAGTGTGGGGGACCAATTAC 240
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; Qy 241 AACCCCTCCTCAAGAGTCAAGTCAACATTTCAACAGACAGCTCCAAGAACCAAGTTCCTCC 300
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; Db 463 TCCAGGAGCACCTCCGAGAGCACAGCGCCCTCTGGGCTGCCTGGTCAAGGACTACTTTCCTCC 522
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; 541 GAACCGGTGACGGTGTCTGTGGAACTTCAGCGGCCCTTCAGCACGCGCGGTGCACACTTTCGG 600
; Qy

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GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain, gamma 4 with the E mutation
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1404
US-08-523-894-9

Query Match 82.2%; Score 1176.2; DB 3; Length 1404;
Best Local Similarity 90.2%; Pred. No. 1.9e-274;
Matches 1291; Conservative 0; Mismatches 113; Indels 27; Gaps 2;

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DB 814 ATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGGTGGAGCTGAGCAGCAACGAGACCT 873
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RESULT 8
US-08-488-376-17
; Sequence 17, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-08-488-376-17
Query Match 79.3%; Score 1134.8; DB 1; Length 1428;
Best Local Similarity 89.0%; Pred. No. 1.8e-264;
Matches 1262; Conservative 0; Mismatches 147; Indels 9; Gaps 3;
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QY 914 ACTGTGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGT 973
Db 911 ACTGTGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGT 970
QY 974 ACAACAGCAGTACCGTGTGGTGTGAGTGTCTCAGCGTCTGTGCAACAGGACTGGCTGAATG 1033
Db 971 ACAACAGCAGTACCGTGTGGTGTGAGTGTCTCAGCGTCTGTGCAACAGGAGTGGCTGAATG 1030
QY 1034 GCAAGGAGTACAGTGCAGGTCTCCAAAGAACCTCCAGCCCGCCATCGAGAAACCA 1093
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QY 1094 TCTCCAAAGCCAAAGGAGCCCGAGAACACAGGTGTACACCTGTCGCCCGCCATCCCGGG 1153
Db 1091 TCTCCAAAGCCAAAGGAGCCCGAGAACACAGGTGTACACCTGTCGCCCGCCATCCCGGG 1150
QY 1154 ATGAGTGTACCAAGAACCAAGGTGAGCTGAGCTGTGTGTCAAGAGCTTCTATCCAGCG 1213
Db 1151 ATGAGTGTACCAAGAACCAAGGTGAGCTGAGCTGTGTGTCAAGAGCTTCTATCCAGCG 1210
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Qy	554	TGTCGTGGAATCAGGCGCCCTGACACAGCGCGTGACACCTTCCCGGTGCTCTACAGT	613
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Db	731	AGCCAAATCTTGTGCAAAACTCACACATGCCCCACCGTGCCAGCACCTTGAACCTCTCTGG	790
Qy	794	GGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGCACCCCTCATGATCTCCCGGA	853
Db	791	GGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGCACCCCTCATGATCTCCCGGA	850
Qy	854	CCCTGAGGTCACTATGCGTGGTGGTGAGCGTGAAGCCCAAGAGCCCTGAGGTCAAGTTCA	913
Db	851	CCCTGAGGTCACTATGCGTGGTGGTGAGCGTGAAGCCCAAGAGCCCTGAGGTCAAGTTCA	910
Qy	914	ACTGGTACGTGGACGGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGT	973
Db	911	ACTGGTACGTGGACGGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGT	970
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Db	971	ACAAACAGCAGTACCGTGTGGTCAGCGTCTCTCACCGTCTGCACAGGAGTGGCTGAATG	1030
Qy	1034	GCAAGGATACAGTGAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCA	1093
Db	1031	GCAAGGATACAGTGAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCA	1090
Qy	1094	TCTCCAAAGCCAAAGGCGACCCCGAACCACAGGTGTACACCTGCCCCCATCCCGGG	1153
Db	1091	TCTCCAAAGCCAAAGGCGACCCCGAACCACAGGTGTACACCTGCCCCCATCCCGGG	1150
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Db	1151	ATGAGCTGACCAAGAAACAGGTGACCTGCTCTGGTCAAGGCTTCTATCCACGCG	1210
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Qy	1274	CCGTGCTGGAATCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGCA	1333
Db	1271	CCGTGCTGGAATCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGCA	1330
Qy	1334	GGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCT	1393
Db	1331	GGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCT	1390
Qy	1394	ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1391	ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA	1428

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